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Om protein - protein search, using sw model

Run on: February 14, 2006, 17:53:18 ; Search time 45 Seconds (without alignments)

Perfect score: 852

Title: US-10-612-012-2

Sequence: 1 MSSSPVQIPLRPLLTHE.....AAFDGGFTVKTRPGILNSKL 852

Scoring table: Oligo Gapext 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 10

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*
1: PIR1:/*
2: PIR2:/*
3: PIR3:/*
4: PIR4:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	17	2.0	774	2	BB4031	ATP-dependent prot endopeptidase La (
2	17	2.0	795	1	AF0322	endopeptidase La (
3	16	1.9	784	2	AC0383	endopeptidase La (
4	16	1.9	875	2	TO9142	endopeptidase La (
5	15	1.8	779	1	BA42375	endopeptidase La (
6	14	1.6	798	2	GB3420	Lon protease PAL endopeptidase La (
7	14	1.6	827	1	AC36895	ATP-dependent seri hypothetical prote
8	14	1.6	848	2	CB2712	ATP-dependent Lon
9	13	1.5	773	2	TO7382	probable ATP-depend
10	13	1.5	778	2	BB97224	endopeptidase La (
11	13	1.5	799	2	AF6956	ATP-dependent prot
12	13	1.5	799	2	PF8549	probable ATP-depend
13	13	1.5	817	1	AA9844	endopeptidase La (
14	13	1.5	821	2	BT75330	ATP-dependent prot
15	13	1.5	885	1	AT0321	endopeptidase La (
16	13	1.5	964	1	TO4325	probable ATP-depend
17	12	1.4	784	1	SA42270	endopeptidase La (
18	12	1.4	784	1	SP2212	probable ATP-depend
19	12	1.4	784	2	AF0558	ATP-dependent prot
20	12	1.4	784	2	BB0690	probable ATP-depend
21	12	1.4	787	2	AT2230	probable ATP-depend
22	12	1.4	799	2	AF5541	probable ATP-depend
23	12	1.4	805	2	CB2731	probable ATP-depend
24	12	1.4	805	2	CG7512	probable ATP-depend
25	12	1.4	810	1	JG6045	probable ATP-depend
26	12	1.4	820	2	HH1106	probable ATP-depend
27	12	1.4	820	2	HH1908	probable ATP-depend
28	12	1.4	881	1	BT7316	probable ATP-depend
	12	1.4	1067	1	SE2421	probable ATP-depend

Total number of hits satisfying chosen parameters: 50

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_80:*

1: PIR1:/*
2: PIR2:/*
3: PIR3:/*
4: PIR4:/*

RESULT 1
BB4031
ATP-dependent proteinase La 1 (lon) (class III heat-shock protein) lonA [Imported] - Bacillus halodurans C;Species: Bacillus halodurans C;Accession: BB4031 C;Text_change: 09-Jul-2004 C;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Accession: BB4031 A;Status: Preliminary A;Molecule type: DNA A;Cross-references: UNIPROT:Q8K8P6; UNIPARC:UPI0000040AD; GB:AP001517; GB:BA000004; NI: C;Genetic: A;Gene: lonA C;Superfamily: ATP-dependent Lon protease

Query Match 2.0% Score 17; DB 2; Length 74; Best local Similarity 100.0%; Pred. No. 4.6e-08; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0; :

Qy 453 GDPAAALLEVLDPQNH 469 Db 433 GDPAAALLEVLDPQNH 449

RESULT 2
AT0322
endopeptidase La (EC 3.4.21.53) - Aquifex aeolicus N;Alternate names: ATP-dependent proteinase lon; ATP-dependent serine proteinase La N;Contains: adenosine triphosphatase (EC 3.6.1.3)
C;Species: Aquifex aeolicus C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 C;Accession: AT0322 C;Status: nucleic acid sequence not shown E;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Or V; Nature 392, 353-358, 1998 A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus A;Cross-references: UNIPROT:O66605; UNIPARC:UPI00000562D8; GB:AE000680; NID:9337320 A;Experimental source: strain VFS C;Genetics: This allosteric enzyme catalyzes the hydrolysis of large proteins in the presence of ATP. A;Molecule type: DNA A;Residues: 1-774 <STOP> A;Gene: lon C;Superfamily: ATP-dependent Lon protease

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 14, 2006, 17:49:34 ; Search time 189 Seconds
 (without alignments)
 1980.692 Million cell updates/sec

Title: US-10-612-012-2

Perfect score: 852

Sequence: 1 MSSVSPIQIPIRSRLPLILTHE.....AAFDGGGETVKTRPGLLNSKL 852

Scoring table: ORIGO

Gapop 60.0 , Gapext 60.0

searched: 2443163 seqs, 439378781 residues

word size : 10

Total number of hits satisfying chosen parameters: 146

minimum DB seq length: 0
maximum DB seq length: 1000000000

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DEFINITION

ABG32363 ID ABG32363 standard; protein; 852

ABG32363 ;
 AC XX DT 15-NOV-2002 (first entry)
 XX Human ATP-dependent protease.
 DB XX

8: generated2004s:*

9: generated2005s:*

IMMATES

Result No.	Score	Query Match	Length	DB	ID	Description
1	852	100.0	852	5	ABG32363	Human ATP
2	852	100.0	852	7	ADM56266	Human ATP
3	852	100.0	852	9	ADY85873	Human pro
4	815	95.7	852	4	AAB47562	Protease
5	815	95.7	852	7	ADC10040	Human
6	714	83.8	852	4	ARM93785	Human pol
7	714	83.8	852	5	ABP69443	Human pol
8	714	83.8	852	8	ADL31771	Human pro
9	693	81.3	693	7	ADJ70423	Human hea
10	581	68.2	581	4	AAB95332	Human pro
11	581	68.2	581	4	AAB99179	Human ATP
12	470	55.2	571	4	AAB94288	Human pro
13	432	50.7	432	4	AAB97167	Human pro
14	432	50.7	432	4	AEE11085	Human ATP
15	421	49.4	433	6	ABU11611	MDD
16	379	44.5	581	8	ADP08563	Human pro
17	331	38.8	423	4	AAU17175	Novel sig
18	331	38.8	423	7	ADB94683	Human nov
19	215	25.2	228	4	AAU17371	Novel sig
20	215	25.2	228	7	ADB94079	Human nov
21	195	22.9	391	5	ABBB89248	Human pol
22	160	18.8	160	8	ADP55489	Human PRO
23	113	13.8	118	4	AAB01658	Human gen
24	85	10.0	85	8	ABO57485	Human

21-DEC-2000; 2000US-00741150.
22-NOV-2000; 2000US-0252410P.

PA (KATC) LAN C.
PA (SHRO) SHAO W.
PA (KETC) KETCHUM K. A.
PA (DFRA) DI FRANCESCO V.
PA (BEAS) BEASLEY E. M.
XX

XX WPI: 2002-625469/68.
DR N-PSDB; ABK90887, ABK90888.
XX New human ATP-dependent peptides and encoding nucleic acids, useful for
PTT diagnosing, preventing and/or treating disorders like cancer, e.g.,
PTT retinoblastomas, melanomas, endometrial and ovarian adenocarcinomas and

Schizophrenia.

OM protein - protein search, using sw model

Run on: February 14, 2006, 17:58:02 ; Search time 169 Seconds
(without alignment) 2106.453 Million cell updates/sec

Title: US-10-612-012-2

Perfect score: 852

Sequence: 1 MSVSPIQTPSRPLPLTH. AAFDGSIFTVKTRPGLNSKL 852

Scoring table: Oligo Gapext 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size : 10

Total number of hits satisfying chosen parameters: 124

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published_Applications_AA_Main.*

1: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US08_PUBCOMB.pep:*

2: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US08_PUBCOMB.pep:*

3: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US10_PUBCOMB.pep:*

4: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US10_PUBCOMB.pep:*

5: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US11_PUBCOMB.pep:*

6: /cmn2_6_ptodata/1/pubpaa/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	852	100.0	852	3 US-09-741-150-2	Sequence 2, Appli
2	852	100.0	852	5 US-10-612-012-2	Sequence 2, Appli
3	815	95.7	852	5 US-10-239-332-4	Sequence 4, Appli
4	693	81.3	693	4 US-10-408-765A-2229	Sequence 2, Appli
5	432	50.7	432	4 US-10-156-239-44	Sequence 4, Appli
6	331	38.8	423	3 US-09-764-668-940	Sequence 940, Appli
7	215	25.2	228	3 US-09-764-868-336	Sequence 936, Appli
8	195	22.9	391	4 US-10-264-237-1624	Sequence 1624, Appli
9	85	10.0	85	4 US-10-029-386-3119	Sequence 3119, Appli
10	78	9.2	78	3 US-09-864-761-33878	Sequence 33878, Appli
11	50	5.9	50	4 US-10-029-386-31256	Sequence 31256, Appli
12	17	2.0	774	4 US-10-369-493-17386	Sequence 17386, Appli
13	17	2.0	786	4 US-10-369-493-8915	Sequence 8915, Appli
14	15	1.9	795	4 US-10-369-493-20	Sequence 20, Appli
15	16	1.9	670	4 US-10-424-559-183947	Sequence 183947, Appli
16	16	1.9	767	4 US-10-369-493-9794	Sequence 9794, Appli
17	16	1.9	777	4 US-10-369-493-9140	Sequence 9140, Appli
18	16	1.9	784	4 US-10-369-493-21223	Sequence 7814, Appli
19	16	1.9	795	4 US-10-369-493-3527	Sequence 3527, Appli
20	16	1.9	892	4 US-10-369-493-3527	Sequence 3527, Appli
21	15	1.8	280	4 US-10-425-114-45912	Sequence 43912, Appli
22	15	1.8	376	4 US-10-424-559-198007	Sequence 198007, Appli
23	15	1.8	766	4 US-10-369-493-16141	Sequence 16141, Appli
24	15	1.8	768	4 US-10-369-493-15835	Sequence 45835, Appli
25	15	1.8	769	4 US-10-369-493-16622	Sequence 16622, Appli
26	15	1.8	777	4 US-10-369-493-373	Sequence 373, Appli
27	15	1.8	784	4 US-10-282-122A-68623	Sequence 68623, Appli

ALIGNMENTS

RESULT 1
US-09-741-150-2

; Sequence 2, Application US/09/41150

; Publication No. US2002001704A1

; GENERAL INFORMATION:

; APPLICANT: GUESLER, Karl et al

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, HUMAN PROTEASE PROTEINS, AND NUCLEAR ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, HUMAN PROTEASE PROTEINS, AND NUCLEAR ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND

; FILE REFERENCE: C100:09/68

; CURRENT APPLICATION NUMBER: US/09/741,150

; CURRENT FILING DATE: 2000-12-21

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 852

; TYPE: PRT

; ORGANISM: Human

US-09-741-150-2

Query Match 100.0%; Score 852; DB 3; Length 852;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 852; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVSPIQTPSRPLPLTHEGVILPGSTMRTSYDSAHNQLVSRLLKTSLOQSTLGV 60

Db 1 MSVSPIQTPSRPLPLTHEGVILPGSTMRTSYDSAHNQLVSRLLKTSLOQSTLGV 60

QY 61 PNTDPASDQDPLPLHRIGTAAVQVGSNNPKPHYTLLITLGICRFOLVQVKEKYP 120

Db 61 PNTDPASDQDPLPLHRIGTAAVQVGSNNPKPHYTLLITLGICRFOLVQVKEKYP 120

QY 61 PNTDPASDQDPLPLHRIGTAAVQVGSNNPKPHYTLLITLGICRFOLVQVKEKYP 120

Db 61 PNTDPASDQDPLPLHRIGTAAVQVGSNNPKPHYTLLITLGICRFOLVQVKEKYP 120

QY 121 IATFQDLDLPEPNTCKRREBGLSEFPRKAVQLVPLMDPSVPAVAKLRLDSLPR 180

Db 121 IATFQDLDLPEPNTCKRREBGLSEFPRKAVQLVPLMDPSVPAVAKLRLDSLPR 180

QY 181 EAPDILTSIITSNKEQLQILDAVSLERFKQTIPILVQRIQSGKLQLKTRPKQDDDK 240

Db 181 EAPDILTSIITSNKEQLQILDAVSLERFKQTIPILVQRIQSGKLQLKTRPKQDDDK 240

QY 241 RVIAIRPIRRITHISGTLDEDDEDNDNDIVMLLEKKIRTSMSMPOAHKVCKB1KRLK 300

Db 241 RVIAIRPIRRITHISGTLDEDDEDNDNDIVMLLEKKIRTSMSMPOAHKVCKB1KRLK 300

QY 301 PQSHFBYALTRNIVSLAVLWLPWNSSTDLDIARILNDHAYAMEKLKGRVLEYLAVR 360

Db 301 PQSHFBYALTRNIVSLAVLWLPWNSSTDLDIARILNDHAYAMEKLKGRVLEYLAVR 360

QY 361 QLKNNLKG1P1LCFYGKPTSYGRSVAKLTGRHRTYVG 420

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נרטיב - דרכין - search - אוניברסיטאות

Digitized by srujanika@gmail.com

February 14, 2006, 17:58:56 ; Search time 17 Seconds
(without Allignment)
657.671 Millions cell updates/sec

title: US-10-6112-012-2
perfect score: 852

Sequence: I MSSVSPIQIIPSRLPPLLTHE: AAFDGGFTVKIREGLLNSRL 852

Scoring Table: OLIGO

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OR : ASTRA

total number of hits satisfying chosen parameters:

minimum DB seq length: 0

ללא עבירות נזקינית. צוותי צבאיים צוותים צבאיים.

Table 45 summarizes the findings of this study.

Published Applications_AA_New
Database :

2: /cgn2_6/ptodata/1/pubpaa/us06_new_pub_depl*
3: /cgn2_6/ptodata/1/pubpaa/us06_new_pub_depl*

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7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.PEP:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

הנתקה

Result				Query			Description	
No.	Score	Match	Length	DB	ID			
1	13	1.5	830	7	US-11-098-686-10393		Sequence 10393, A	
2	12	1.4	804	7	US-11-070-080-18		Sequence 18, App1	
3	12	1.4	820	6	US-11-067-557-4910		Sequence 10, App1	
4	11	1.3	817	7	US-11-098-686-11041		Sequence 11041	

ALIGNMENTS

Sequence 10393, Application US/11098686
Publication No. US2006024696A1
* * * * *
GENERAL INFORMATION:
APPLICANT: KAPUR, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEAR ACID AND POLYPEPTIDE SEQUENCES
TITLE OF INVENTION: FROM LAWONIA INTRACELLULARIS AND METHODS OF USING
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098,686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 1-1432

```

; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 10393
; LENGTH: 830
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10393

Query Match          1.5%;  Score 13;
Best Local Similarity 100.0%; Pred. No.
Matches   13;  Conservative 0;  Mismatch
Qy          685 LRGQLGDMKESA 697
Db          667 LRGQLGDMKESA 679

RESULT 2
US-11-070-080-18
; Sequence 18, Application US/11070080
; Publication No. US20050287625A1
; GENERAL INFORMATION:
; APPLICANT: Ye, Rick W.
; APPLICANT: Miller, Edward S.
; TITLE OF INVENTION: PROCESS FOR EXPRESSION
; OF BACTERIA THROUGH CHROMO
; TITLES OF INVENTION: BACTERIA THROUGH CHROMO
; FILE REFERENCE: CL-2443 US NA
; CURRENT APPLICATION NUMBER: US/11/070, 080
; CURRENT FILING DATE: 2005-03-02
; PRIOR APPLICATION NUMBER: US 60/550385
; PRIOR FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 804
; TYPE: PRT
; ORGANISM: Methyloimonas sp. 16a
US-11-070-080-18

Query Match          1.4%;  Score 12;
Best Local Similarity 100.0%; Pred. No.
Matches   12;  Conservative 0;  Mismatch
Qy          458 ALLEVLDEPEQNH 469
Db          440 ALLEVLDEPEQNH 451

RESULT 3
US-10-467-657-4910
; Sequence 4910, Application US/10467657
; Publication No. US2005260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin9, version 1.04
; SEQ ID NO 4910
; LENGTH: 820
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4910

Query Match          1.4%;  Score 12;

```


